

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 1, line 4, with the following paragraph:

This application is a continuation-in-part of U.S. Patent Application Serial No. 09/659,173 "Calibration Of Molecular Array Data", filed September 11, 2000, by Wolber, et al., from which priority is claimed and which is incorporated herein by reference, now abandoned.

Please replace the paragraph beginning on page 29, line 1, with the following paragraph:

Experimental verification of the first of the four above-described embodiments employing poly(A) oligonucleotide probes was obtained as follows. Purified mRNA from human K-562 cells was amplified and labeled to produce labeled cRNA target molecules by a method disclosed in U.S. Patent No. 6,132,997 ~~U.S. Patent Application No. 09/322692~~, entitled "A Method for Linear Amplification of Heterogeneous mRNA" and filed May 28, 1999. A sample solution containing equal concentrations of Cy3- and Cy5-labeled K-562 cRNA was prepared and applied to two molecular arrays, each containing probes to about 100 human reference mRNA sequences. Approximately nine probes for each reference sequence were included in the two molecular arrays, each probe redundantly included in a sufficient number of different features to fill the molecular arrays. In addition, the two molecular arrays also contained four features per array containing each of the poly(A) normalization probes shown in Table 8, below:

Please replace the paragraph beginning on page 32, line 27, with the following paragraph:

Additional experimental verification, using stylized human repeat sequences for normalization, was obtained, as follows. The same *in situ*-synthesized oligonucleotide array was used for all experiments. The array was designed by tiling 60-mer probes across 80 human sequences, with a spacing of 50 nucleotides (i.e. probes to bases 1-60, 51-110, 101-160, ..., to the end of the gene). The same sequences used to design the array were also processed using Repeat Masker (see

~~<http://repeatmasker.genome.washington.edu/>~~), a computer program that identifies and marks low complexity, species-independent sub-sequences and stylized, species dependent repeat sequences. The Repeat Masker settings appropriate to human sequences were selected. The resulting masked sequences were compared to the tiling probes, and used to prepare a table that set a binary flag for each probe to one of the values: (1) TRUE, if the probe overlapped any masked bases; and (2) FALSE, otherwise. This table was used during subsequent visualization of the experimental results.

Please replace the paragraph beginning on page 33, line 24, with the following paragraph:

The arrays were hybridized, washed and scanned according to the manufacturer's instructions (see ~~<http://www.chem.agilent.com/Scripts/PCol.asp?IPage=494>~~). The resulting data was loaded into a Microsoft Access 2000 database, and results were visualized using either Spotfire Decision Site or Microsoft Excel 2000 software.

Please replace the paragraph beginning on page 33, line 29, with the following paragraph:

A first example involves the human fragile X mental retardation gene. The human fragile X mental retardation gene, FMR1 (see ~~<http://www.ncbi.nlm.nih.gov/LocusLink/LocRpt.cgi?l=2332>~~ for details) is known to be enriched in C/G-rich nucleotide triplet repeats at the 5'-end of the sequence encoding the gene's mature mRNA transcript. Expansion of these triplets due to mistakes during DNA replication gives rise to fragile X syndrome, one of the leading causes of genetically determined mental retardation in humans. This mRNA was profiled in HeLa and K562 cells, via the microarrays and experimental protocols described above. The results of these experiments for probes to the 5'-end of the FMR1 mRNA are summarized in Figures 13 and 14.

Please replace the paragraph beginning on page 35, line 12, with the following paragraph:

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